



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Morin, Gregg B.
Allsopp, Richard
DePinho, Ronald
Greenberg, Roger
- (ii) TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase
- (iii) NUMBER OF SEQUENCES: 101
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/042,460
(B) FILING DATE: 16-MAR-1998
(C) CLASSIFICATION:
- 24 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/724,643
(B) FILING DATE: 01-OCT-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/844,419
(B) FILING DATE: 18-APR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/846,017
(B) FILING DATE: 25-APR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/851,843
(B) FILING DATE: 06-MAY-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/854,050
(B) FILING DATE: 09-MAY-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/911,312
(B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/912,951
(B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/915,503
(B) FILING DATE: 14-AUG-1997

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- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/US97/17618
 - (B) FILING DATE: 01-OCT-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/US97/17885
 - (B) FILING DATE: 01-OCT-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/974,549
 - (B) FILING DATE: 19-NOV-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/974,584
 - (B) FILING DATE: 19-NOV-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/979,742
 - (B) FILING DATE: 26-NOV-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Einhorn, Gregory P.
 - (B) REGISTRATION NUMBER: 38,440
 - (C) REFERENCE/DOCKET NUMBER: 015389-003110US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 576-0200
 - (B) TELEFAX: (415) 576-0300
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..3496
 - (D) OTHER INFORMATION: /note= "mouse telomerase reverse transcriptase (mTRT) cDNA clone"
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 10..3435
 - (D) OTHER INFORMATION: /note= "mouse telomerase reverse transcriptase (mTRT) cDNA"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 39..3404
 - (D) OTHER INFORMATION: /product= "mouse telomerase reverse transcriptase (mTRT)"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGG TGGGAGGCC ATCCCGGCCT TGAGCACA ATG ACC CGC GCT CCT
 Met Thr Arg Ala Pro
 1 5

CGT TGC CCC GCG GTG CGC TCT CTG CTG CGC AGC CGA TAC CGG GAG GTG Arg Cys Pro Ala Val Arg Ser Leu Leu Arg Ser Arg Tyr Arg Glu Val 10 15 20	101
TGG CCG CTG GCA ACC TTT GTG CGG CGC CTG GGG CCC GAG GGC AGG CGG Trp Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Glu Gly Arg Arg 25 30 35	149
CTT GTG CAA CCC GGG GAC CCG AAG ATC TAC CGC ACT TTG GTT GCC CAA Leu Val Gln Pro Gly Asp Pro Lys Ile Tyr Arg Thr Leu Val Ala Gln 40 45 50	197
TGC CTA GTG TGC ATG CAC TGG GGC TCA CAG CCT CCA CCT GCC GAC CTT Cys Leu Val Cys Met His Trp Gly Ser Gln Pro Pro Pro Ala Asp Leu 55 60 65	245
TCC TTC CAC CAG GTG TCA TCC CTG AAA GAG CTG GTG GCC AGG GTT GTG Ser Phe His Gln Val Ser Ser Leu Lys Glu Leu Val Ala Arg Val Val 70 75 80 85	293
CAG AGA CTC TGC GAG CGC AAC GAG AGA AAC GTG CTG GCT TTT GGC TTT Gln Arg Leu Cys Glu Arg Asn Glu Arg Asn Val Leu Ala Phe Gly Phe 90 95 100	341
GAG CTG CTT AAC GAG GCC AGA GGC GGG CCT CCC ATG GCC TTC ACT AGT Glu Leu Leu Asn Glu Ala Arg Gly Gly Pro Pro Met Ala Phe Thr Ser 105 110 115	389
AGC GTG CGT AGC TAC TTG CCC AAC ACT GTT ATT GAG ACC CTG CGT GTC Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Ile Glu Thr Leu Arg Val 120 125 130	437
AGT GGT GCA TGG ATG CTA CTG TTG AGC CGA GTG GGC GAC GAC CTG CTG Ser Gly Ala Trp Met Leu Leu Leu Ser Arg Val Gly Asp Asp Leu Leu 135 140 145	485
GTC TAC CTG CTG GCA CAC TGT GCT CTT TAT CTT CTG GTG CCC CCC AGC Val Tyr Leu Leu Ala His Cys Ala Leu Tyr Leu Leu Val Pro Pro Ser 150 155 160 165	533
TGT GCC TAC CAG GTG TGT GGG TCT CCC CTG TAC CAA ATT TGT GCC ACC Cys Ala Tyr Gln Val Cys Gly Ser Pro Leu Tyr Gln Ile Cys Ala Thr 170 175 180	581
ACG GAT ATC TGG CCC TCT GTG TCC GCT AGT TAC AGG CCC ACC CGA CCC Thr Asp Ile Trp Pro Ser Val Ser Ala Ser Tyr Arg Pro Thr Arg Pro 185 190 195	629
GTG GGC AGG AAT TTC ACT AAC CTT AGG TTC TTA CAA CAG ATC AAG AGC Val Gly Arg Asn Phe Thr Asn Leu Arg Phe Leu Gln Gln Ile Lys Ser 200 205 210	677
AGT AGT CGC CAG GAA GCA CCG AAA CCC CTG GCC TTG CCA TCT CGA GGT Ser Ser Arg Gln Glu Ala Pro Lys Pro Leu Ala Leu Pro Ser Arg Gly 215 220 225	725
ACA AAG AGG CAT CTG AGT CTC ACC AGT ACA AGT GTG CCT TCA GCT AAG Thr Lys Arg His Leu Ser Leu Thr Ser Thr Ser Val Pro Ser Ala Lys 230 235 240 245	773
AAG GCC AGA TGC TAT CCT GTC CCG AGA GTG GAG GAG GGA CCC CAC AGG Lys Ala Arg Cys Tyr Pro Val Pro Arg Val Glu Glu Gly Pro His Arg 250 255 260	821
CAG GTG CTA CCA ACC CCA TCA GGC AAA TCA TGG GTG CCA AGT CCT GCT Gln Val Leu Pro Thr Pro Ser Gly Lys Ser Trp Val Pro Ser Pro Ala 265 270 275	869

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AAG GTG TCT GAC CTG AGT CTC TCT GGG TCG GTG TGC TGT AAA CAC AAG Lys Val Ser Asp Leu Ser Leu Ser Gly Ser Val Cys Cys Lys His Lys 295 300 305	965
CCC AGC TCC ACA TCT CTG CTG TCA CCA CCC CGC CAA AAT GCC TTT CAG Pro Ser Ser Thr Ser Leu Leu Ser Pro Pro Arg Gln Asn Ala Phe Gln 310 315 320 325	1013
CTC AGG CCA TTT ATT GAG ACC AGA CAT TTC CTT TAC TCC AGG GGA GAT Leu Arg Pro Phe Ile Glu Thr Arg His Phe Leu Tyr Ser Arg Gly Asp 330 335 340	1061
GGC CAA GAG CGT CTA AAC CCC TCA TTC CTA CTC AGC AAC CTC CAG CCT Gly Gln Glu Arg Leu Asn Pro Ser Phe Leu Leu Ser Asn Leu Gln Pro 345 350 355	1109
AAC TTG ACT GGG GCC AGG AGA CTG GTG GAG ATC ATC TTT CTG GGC TCA Asn Leu Thr Gly Ala Arg Arg Leu Val Glu Ile Ile Phe Leu Gly Ser 360 365 370	1157
AGG CCT AGG ACA TCA GGA CCA CTC TGC AGG ACA CAC CGT CTA TCG CGT Arg Pro Arg Thr Ser Gly Pro Leu Cys Arg Thr His Arg Leu Ser Arg 375 380 385	1205
CGA TAC TGG CAG ATG CGG CCC CTG TTC CAA CAG CTG CTG GTG AAC CAT Arg Tyr Trp Gln Met Arg Pro Leu Phe Gln Gln Leu Leu Val Asn His 390 395 400 405	1253
GCA GAG TGC CAA TAT GTC AGA CTC CTC AGG TCA CAT TGC AGG TTT CGA Ala Glu Cys Gln Tyr Val Arg Leu Leu Arg Ser His Cys Arg Phe Arg 410 415 420	1301
ACA GCA AAC CAA CAG GTG ACA GAT GCC TTG AAC ACC AGC CCA CCG CAC Thr Ala Asn Gln Gln Val Thr Asp Ala Leu Asn Thr Ser Pro Pro His 425 430 435	1349
CTC ATG GAT TTG CTC CGC CTG CAC AGC AGT CCC TGG CAG GTA TAT GGT Leu Met Asp Leu Leu Arg Leu His Ser Ser Pro Trp Gln Val Tyr Gly 440 445 450	1397
TTT CTT CGG GCC TGT CTC TGC AAG GTG GTG TCT GCT AGT CTC TGG GGT Phe Leu Arg Ala Cys Leu Cys Lys Val Val Ser Ala Ser Leu Trp Gly 455 460 465	1445
ACC AGG CAC AAT GAG CGC CGC TTC TTT AAG AAC TTA AAG AAG TTC ATC Thr Arg His Asn Glu Arg Arg Phe Phe Lys Asn Leu Lys Lys Phe Ile 470 475 480 485	1493
TCG TTG GGG AAA TAC GGC AAG CTA TCA CTG CAG GAA CTG ATG TGG AAG Ser Leu Gly Lys Tyr Gly Lys Leu Ser Leu Gln Glu Leu Met Trp Lys 490 495 500	1541
ATG AAA GTA GAG GAT TGC CAC TGG CTC CGC AGC AGC CCG GGG AAG GAC Met Lys Val Glu Asp Cys His Trp Leu Arg Ser Ser Pro Gly Lys Asp 505 510 515	1589
CGT GTC CCC GCT GCA GAG CAC CGT CTG AGG GAG AGG ATC CTG GCT ACG Arg Val Pro Ala Ala Glu His Arg Leu Arg Glu Arg Ile Leu Ala Thr 520 525 530	1637
TTC CTG TTC TGG CTG ATG GAC ACA TAC GTG GTA CAG CTG CTT AGG TCA Phe Leu Phe Trp Leu Met Asp Thr Tyr Val Val Gln Leu Leu Arg Ser 535 540 545	1685

TTC TTT TAC ATC ACA GAG AGC ACA TTC CAG AAG AAC AGG CTC TTC TTC Phe Phe Tyr Ile Thr Glu Ser Thr Phe Gln Lys Asn Arg Leu Phe Phe 550 555 560 565	1733
TAC CGT AAG AGT GTG TGG AGC AAG CTG CAG AGC ATT GGA GTC AGG CAA Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Val Arg Gln 570 575 580	1781
CAC CTT GAG AGA GTG CGG CTA CGG GAG CTG TCA CAA GAG GAG GTC AGG His Leu Glu Arg Val Arg Leu Arg Glu Leu Ser Gln Glu Glu Val Arg 585 590 595	1829
CAT CAC CAG GAC ACC TGG CTA GCC ATG CCC ATC TGC AGA CTG CGC TTC His His Gln Asp Thr Trp Leu Ala Met Pro Ile Cys Arg Leu Arg Phe 600 605 610	1877
ATC CCC AAG CCC AAC GGC CTG CGG CCC ATT GTG AAC ATG AGT TAT AGC Ile Pro Lys Pro Asn Gly Leu Arg Pro Ile Val Asn Met Ser Tyr Ser 615 620 625	1925
ATG GGT ACC AGA GCT TTG GGC AGA AGG AAG CAG GCC CAG CAT TTC ACC Met Gly Thr Arg Ala Leu Gly Arg Arg Lys Gln Ala Gln His Phe Thr 630 635 640 645	1973
CAG CGT CTC AAG ACT CTC TTC AGC ATG CTC AAC TAT GAG CGG ACA AAA Gln Arg Leu Lys Thr Leu Phe Ser Met Leu Asn Tyr Glu Arg Thr Lys 650 655 660	2021
CAT CCT CAC CTT ATG GGG TCT TCT GTA CTG GGT ATG AAT GAC ATC TAC His Pro His Leu Met Gly Ser Ser Val Leu Gly Met Asn Asp Ile Tyr 665 670 675	2069
AGG ACC TGG CGG GCC TTT GTG CTG CGT GTG CGT GCT CTG GAC CAG ACA Arg Thr Trp Arg Ala Phe Val Leu Arg Val Arg Ala Leu Asp Gln Thr 680 685 690	2117
CCC AGG ATG TAC TTT GTT AAG GCA GAT GTG ACC GGG GCC TAT GAT GCC Pro Arg Met Tyr Phe Val Lys Ala Asp Val Thr Gly Ala Tyr Asp Ala 695 700 705	2165
ATC CCC CAG GGT AAG CTG GTG GAG GTT GTT GCC AAT ATG ATC AGG CAC Ile Pro Gln Gly Lys Leu Val Glu Val Val Ala Asn Met Ile Arg His 710 715 720 725	2213
TCG GAG AGC ACG TAC TGT ATC CGC CAG TAT GCA GTG GTC CGG AGA GAT Ser Glu Ser Thr Tyr Cys Ile Arg Gln Tyr Ala Val Val Arg Arg Asp 730 735 740	2261
AGC CAA GGC CAA GTC CAC AAG TCC TTT AGG AGA CAG GTC ACC ACC CTC Ser Gln Gly Gln Val His Lys Ser Phe Arg Arg Gln Val Thr Thr Leu 745 750 755	2309
TCT GAC CTC CAG CCA TAC ATG GGC CAG TTC CTT AAG CAT CTG CAG GAT Ser Asp Leu Gln Pro Tyr Met Gly Gln Phe Leu Lys His Leu Gln Asp 760 765 770	2357
TCA GAT GCC AGT GCA CTG AGG AAC TCC GTT GTC ATC GAG CAG AGC ATC Ser Asp Ala Ser Ala Leu Arg Asn Ser Val Val Ile Glu Gln Ser Ile 775 780 785	2405
TCT ATG AAT GAG AGC AGC AGC AGC CTG TTT GAC TTC TTC CTG CAC TTC Ser Met Asn Glu Ser Ser Ser Ser Leu Phe Asp Phe Phe Leu His Phe 790 795 800 805	2453
CTG CGT CAC AGT GTC GTA AAG ATT GGT GAC AGG TGC TAT ACG CAG TGC Leu Arg His Ser Val Val Lys Ile Gly Asp Arg Cys Tyr Thr Gln Cys 810 815 820	2501

CAG GGC ATC CCC CAG GGC TCC AGC CTA TCC ACC CTG CTC TGC AGT CTG Gln Gly Ile Pro Gln Gly Ser Ser Leu Ser Thr Leu Leu Cys Ser Leu 825 830 835	2549
TGT TTC GGA GAC ATG GAG AAC AAG CTG TTT GCT GAG GTG CAG CGG GAT Cys Phe Gly Asp Met Glu Asn Lys Leu Phe Ala Glu Val Gln Arg Asp 840 845 850	2597
GGG TTG CTT TTA CGT TTT GTT GAT GAC TTT CTG TTG GTG ACG CCT CAC Gly Leu Leu Leu Arg Phe Val Asp Asp Phe Leu Leu Val Thr Pro His 855 860 865	2645
TTG GAC CAA GCA AAA ACC TTC CTC AGC ACC CTG GTC CAT GGC GTT CCT Leu Asp Gln Ala Lys Thr Phe Leu Ser Thr Leu Val His Gly Val Pro 870 875 880 885	2693
GAG TAT GGG TGC ATG ATA AAC TTG CAG AAG ACA GTG GTG AAC TTC CCT Glu Tyr Gly Cys Met Ile Asn Leu Gln Lys Thr Val Val Asn Phe Pro 890 895 900	2741
GTG GAG CCT GGT ACC CTG GGT GGT GCA GCT CCA TAC CAG CTG CCT GCT Val Glu Pro Gly Thr Leu Gly Gly Ala Ala Pro Tyr Gln Leu Pro Ala 905 910 915	2789
CAC TGC CTG TTT CCC TGG TGT GGC TTG CTG CTG GAC ACT CAG ACT TTG His Cys Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Gln Thr Leu 920 925 930	2837
GAG GTG TTC TGT GAC TAC TCA GGT TAT GCC CAG ACC TCA ATT AAG ACG Glu Val Phe Cys Asp Tyr Ser Gly Tyr Ala Gln Thr Ser Ile Lys Thr 935 940 945	2885
AGC CTC ACC TTC CAG AGT GTC TTC AAA GCT GGG AAG ACC ATG CGG AAC Ser Leu Thr Phe Gln Ser Val Phe Lys Ala Gly Lys Thr Met Arg Asn 950 955 960 965	2933
AAG CTC CTG TCG GTC TTG CGG TTG AAG TGT CAC GGT CTA TTT CTA GAC Lys Leu Leu Ser Val Leu Arg Leu Lys Cys His Gly Leu Phe Leu Asp 970 975 980	2981
TTG CAG GTG AAC AGC CTC CAG ACA GTC TGC ATC AAT ATA TAC AAG ATC Leu Gln Val Asn Ser Leu Gln Thr Val Cys Ile Asn Ile Tyr Lys Ile 985 990 995	3029
TTC CTG CTT CAG GCC TAC AGG TTC CAT GCA TGT GTG ATT CAG CTT CCC Phe Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Ile Gln Leu Pro 1000 1005 1010	3077
TTT GAC CAG CGT GTT AGG AAG AAC CTC ACA TTC TTT CTG GGC ATC ATC Phe Asp Gln Arg Val Arg Lys Asn Leu Thr Phe Phe Leu Gly Ile Ile 1015 1020 1025	3125
TCC AGC CAA GCA TCC TGC TGC TAT GCT ATC CTG AAG GTC AAG AAT CCA Ser Ser Gln Ala Ser Cys Cys Tyr Ala Ile Leu Lys Val Lys Asn Pro 1030 1035 1040 1045	3173
GGA ATG ACA CTA AAG GCC TCT GGC TCC TTT CCT CCT GAA GCC GCA CAT Gly Met Thr Leu Lys Ala Ser Gly Ser Phe Pro Pro Glu Ala Ala His 1050 1055 1060	3221
TGG CTC TGC TAC CAG GCC TTC CTG CTC AAG CTG GCT GCT CAT TCT GTC Trp Leu Cys Tyr Gln Ala Phe Leu Leu Lys Leu Ala Ala His Ser Val 1065 1070 1075	3269
ATC TAC AAA TGT CTC CTG GGA CCT CTG AGG ACA GCC CAA AAA CTG CTG Ile Tyr Lys Cys Leu Leu Gly Pro Leu Arg Thr Ala Gln Lys Leu Leu 1080 1085 1090	3317

TGC CGG AAG CTC CCA GAG GCG ACA ATG ACC ATC CTT AAA GCT GCA GCT 3365
 Cys Arg Lys Leu Pro Glu Ala Thr Met Thr Ile Leu Lys Ala Ala Ala
 1095 1100 1105

GAC CCA GCC CTA AGC ACA GAC TTT CAG ACC ATT TTG GAC TAACCCTGTC 3414
 Asp Pro Ala Leu Ser Thr Asp Phe Gln Thr Ile Leu Asp
 1110 1115 1120

TCCTTCCGCT AGATGAACAT GAAGGGCGAA TTCCAGCACA CTGGCGGCCG TTACTAGTGG 3474
 ATCCGAGCTC GGTACCAAGC TT 3496

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Arg Ala Pro Arg Cys Pro Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
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 Pro Glu Gly Arg Arg Leu Val Gln Pro Gly Asp Pro Lys Ile Tyr Arg
 35 40 45
 Thr Leu Val Ala Gln Cys Leu Val Cys Met His Trp Gly Ser Gln Pro
 50 55 60
 Pro Pro Ala Asp Leu Ser Phe His Gln Val Ser Ser Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Val Gln Arg Leu Cys Glu Arg Asn Glu Arg Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Glu Leu Leu Asn Glu Ala Arg Gly Gly Pro Pro
 100 105 110
 Met Ala Phe Thr Ser Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Ile
 115 120 125
 Glu Thr Leu Arg Val Ser Gly Ala Trp Met Leu Leu Leu Ser Arg Val
 130 135 140
 Gly Asp Asp Leu Leu Val Tyr Leu Leu Ala His Cys Ala Leu Tyr Leu
 145 150 155 160
 Leu Val Pro Pro Ser Cys Ala Tyr Gln Val Cys Gly Ser Pro Leu Tyr
 165 170 175
 Gln Ile Cys Ala Thr Thr Asp Ile Trp Pro Ser Val Ser Ala Ser Tyr
 180 185 190
 Arg Pro Thr Arg Pro Val Gly Arg Asn Phe Thr Asn Leu Arg Phe Leu
 195 200 205
 Gln Gln Ile Lys Ser Ser Ser Arg Gln Glu Ala Pro Lys Pro Leu Ala
 210 215 220

Leu Pro Ser Arg Gly Thr Lys Arg His Leu Ser Leu Thr Ser Thr Ser
 225 230 235 240
 Val Pro Ser Ala Lys Lys Ala Arg Cys Tyr Pro Val Pro Arg Val Glu
 245 250 255
 Glu Gly Pro His Arg Gln Val Leu Pro Thr Pro Ser Gly Lys Ser Trp
 260 265 270
 Val Pro Ser Pro Ala Arg Ser Pro Glu Val Pro Thr Ala Glu Lys Asp
 275 280 285
 Leu Ser Ser Lys Gly Lys Val Ser Asp Leu Ser Leu Ser Gly Ser Val
 290 295 300
 Cys Cys Lys His Lys Pro Ser Ser Thr Ser Leu Leu Ser Pro Pro Arg
 305 310 315 320
 Gln Asn Ala Phe Gln Leu Arg Pro Phe Ile Glu Thr Arg His Phe Leu
 325 330 335
 Tyr Ser Arg Gly Asp Gly Gln Glu Arg Leu Asn Pro Ser Phe Leu Leu
 340 345 350
 Ser Asn Leu Gln Pro Asn Leu Thr Gly Ala Arg Arg Leu Val Glu Ile
 355 360 365
 Ile Phe Leu Gly Ser Arg Pro Arg Thr Ser Gly Pro Leu Cys Arg Thr
 370 375 380
 His Arg Leu Ser Arg Arg Tyr Trp Gln Met Arg Pro Leu Phe Gln Gln
 385 390 395 400
 Leu Leu Val Asn His Ala Glu Cys Gln Tyr Val Arg Leu Leu Arg Ser
 405 410 415
 His Cys Arg Phe Arg Thr Ala Asn Gln Gln Val Thr Asp Ala Leu Asn
 420 425 430
 Thr Ser Pro Pro His Leu Met Asp Leu Leu Arg Leu His Ser Ser Pro
 435 440 445
 Trp Gln Val Tyr Gly Phe Leu Arg Ala Cys Leu Cys Lys Val Val Ser
 450 455 460
 Ala Ser Leu Trp Gly Thr Arg His Asn Glu Arg Arg Phe Phe Lys Asn
 465 470 475 480
 Leu Lys Lys Phe Ile Ser Leu Gly Lys Tyr Gly Lys Leu Ser Leu Gln
 485 490 495
 Glu Leu Met Trp Lys Met Lys Val Glu Asp Cys His Trp Leu Arg Ser
 500 505 510
 Ser Pro Gly Lys Asp Arg Val Pro Ala Ala Glu His Arg Leu Arg Glu
 515 520 525
 Arg Ile Leu Ala Thr Phe Leu Phe Trp Leu Met Asp Thr Tyr Val Val
 530 535 540
 Gln Leu Leu Arg Ser Phe Phe Tyr Ile Thr Glu Ser Thr Phe Gln Lys
 545 550 555 560
 Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser
 565 570 575

Ile Gly Val Arg Gln His Leu Glu Arg Val Arg Leu Arg Glu Leu Ser
 580 585 590
 Gln Glu Glu Val Arg His His Gln Asp Thr Trp Leu Ala Met Pro Ile
 595 600 605
 Cys Arg Leu Arg Phe Ile Pro Lys Pro Asn Gly Leu Arg Pro Ile Val
 610 615 620
 Asn Met Ser Tyr Ser Met Gly Thr Arg Ala Leu Gly Arg Arg Lys Gln
 625 630 635 640
 Ala Gln His Phe Thr Gln Arg Leu Lys Thr Leu Phe Ser Met Leu Asn
 645 650 655
 Tyr Glu Arg Thr Lys His Pro His Leu Met Gly Ser Ser Val Leu Gly
 660 665 670
 Met Asn Asp Ile Tyr Arg Thr Trp Arg Ala Phe Val Leu Arg Val Arg
 675 680 685
 Ala Leu Asp Gln Thr Pro Arg Met Tyr Phe Val Lys Ala Asp Val Thr
 690 695 700
 Gly Ala Tyr Asp Ala Ile Pro Gln Gly Lys Leu Val Glu Val Val Ala
 705 710 715 720
 Asn Met Ile Arg His Ser Glu Ser Thr Tyr Cys Ile Arg Gln Tyr Ala
 725 730 735
 Val Val Arg Arg Asp Ser Gln Gly Gln Val His Lys Ser Phe Arg Arg
 740 745 750
 Gln Val Thr Thr Leu Ser Asp Leu Gln Pro Tyr Met Gly Gln Phe Leu
 755 760 765
 Lys His Leu Gln Asp Ser Asp Ala Ser Ala Leu Arg Asn Ser Val Val
 770 775 780
 Ile Glu Gln Ser Ile Ser Met Asn Glu Ser Ser Ser Ser Leu Phe Asp
 785 790 795 800
 Phe Phe Leu His Phe Leu Arg His Ser Val Val Lys Ile Gly Asp Arg
 805 810 815
 Cys Tyr Thr Gln Cys Gln Gly Ile Pro Gln Gly Ser Ser Leu Ser Thr
 820 825 830
 Leu Leu Cys Ser Leu Cys Phe Gly Asp Met Glu Asn Lys Leu Phe Ala
 835 840 845
 Glu Val Gln Arg Asp Gly Leu Leu Leu Arg Phe Val Asp Asp Phe Leu
 850 855 860
 Leu Val Thr Pro His Leu Asp Gln Ala Lys Thr Phe Leu Ser Thr Leu
 865 870 875 880
 Val His Gly Val Pro Glu Tyr Gly Cys Met Ile Asn Leu Gln Lys Thr
 885 890 895
 Val Val Asn Phe Pro Val Glu Pro Gly Thr Leu Gly Gly Ala Ala Pro
 900 905 910
 Tyr Gln Leu Pro Ala His Cys Leu Phe Pro Trp Cys Gly Leu Leu Leu
 915 920 925

Asp Thr Gln Thr Leu Glu Val Phe Cys Asp Tyr Ser Gly Tyr Ala Gln
 930 935 940
 Thr Ser Ile Lys Thr Ser Leu Thr Phe Gln Ser Val Phe Lys Ala Gly
 945 950 955 960
 Lys Thr Met Arg Asn Lys Leu Leu Ser Val Leu Arg Leu Lys Cys His
 965 970 975
 Gly Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Ile
 980 985 990
 Asn Ile Tyr Lys Ile Phe Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 995 1000 1005
 Val Ile Gln Leu Pro Phe Asp Gln Arg Val Arg Lys Asn Leu Thr Phe
 1010 1015 1020
 Phe Leu Gly Ile Ile Ser Ser Gln Ala Ser Cys Cys Tyr Ala Ile Leu
 1025 1030 1035 1040
 Lys Val Lys Asn Pro Gly Met Thr Leu Lys Ala Ser Gly Ser Phe Pro
 1045 1050 1055
 Pro Glu Ala Ala His Trp Leu Cys Tyr Gln Ala Phe Leu Leu Lys Leu
 1060 1065 1070
 Ala Ala His Ser Val Ile Tyr Lys Cys Leu Leu Gly Pro Leu Arg Thr
 1075 1080 1085
 Ala Gln Lys Leu Leu Cys Arg Lys Leu Pro Glu Ala Thr Met Thr Ile
 1090 1095 1100
 Leu Lys Ala Ala Ala Asp Pro Ala Leu Ser Thr Asp Phe Gln Thr Ile
 1105 1110 1115 1120
 Leu Asp

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..1132
 - (D) OTHER INFORMATION: /note= "human telomerase reverse transcriptase (hTRT)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1808
- (D) OTHER INFORMATION: /note= "preliminary sequence of genomic mouse telomerase reverse transcriptase (mTRT) promoter region"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1680
- (D) OTHER INFORMATION: /note= "mouse telomerase reverse transcriptase (mTRT) cDNA start site"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1709
- (D) OTHER INFORMATION: /note= "mouse telomerase reverse transcriptase (mTRT) ORF start site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAGCAGGCC TGTAACACAA AGGTCCTTTT TCCTGGTTTA TCGTGGCTGG TAGACAATTT	60
CCACTTGTTT TCCAATTGAG TTTTCTCTAC TCGGTTGTTA TTGGATTCTG ATGCTTGAAC	120
CCAGGTTGGT AGTCAGCAAG TGCACCCCTT CCTTCTTTTT CTTGGTTTTT TTGAGGCAGG	180
TCTCATTTTG CCCAAGTGGA CCTAAATTTT AGCATGTAGT GGCTGGTTTN GAATGCTTTT	240
TCATCCTGCT NTAATTCCCA AGAGTAGCTA ACAAGTGTGC ACCACCATGC CCCGCGATAT	300
TTTTATTTTT GAGACTGTTT TCTATGCTGG TTTCTTTGGG GAACTACACT AAGGTAGCTT	360
ACAAGTGTGC ACCACCATGC CCCGCGATAT TCTTATTTTT GAGACTGTTT TCTATGCTGG	420
TTTCTTTGGG GAACTACACT AAGGTAGCTT CATTGTTGGC ATAAATTTCT CAGTTCAGGC	480
CCATATCTCT TAAGTAGCAG AACTAAGCCA AATCTTCAAA CAAACCCCTT CAAAAGACT	540
GATGTCCACT AAACGGACTT CTAAATAGC TCCCTGTAAT CCTGAGCATT TACCAAGGCG	600
GCAGACTTCC TATAAGGGAG TAAATATGAA AACGCGCCTG TTCAAATGCT AGGTCGGTGG	660
ATAGAAGCAA TTTCCTCAGA AAGCTGAAGG CACCAAAGGT TATATTTGTT AGCATTTTCA	720
TGTTTGCCAA ACTCAGCTAC AGTAGAGATC ACAGATTCCC TATTTCCAG AGATTCAAAA	780
TTCAGCAGCC CCTCTTAAC TATGGCTCAG AGTCGTGTCA TTACATATGC CCCAACAACA	840

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ACCCCCACCC CTATCCTACC CCCGCCTCAC ACGTGCAAGT ACTATCACAG TTGCCAACCT      900
AGCAGAGCTG CCATCCTAAG GTCGAGGTCG CCGCTTTGGC TGTGTGCACA GGCAAGCGCC      960
CTCACCCAAT GGCCCTGGCC TTGCTATGGG TGCCTGAGTT GAGATGATGC TCTGGACTCT      1020
GAGGTGAAGG CCACTGGAAC AGTGAAAAAA GCTAACGCAG GGCTTTTACC TAGGTCCCCT      1080
TCCTTTGGTG GTGGGTGTTT ACGGAACATA TTTGGGATCT GGAGTGTATG GTCGCACCAC      1140
AATAAAGCCT TAACCTATAT AGTAGAATGT TCAGCTGTAA TCATTAAGAA CTGAGATTGC      1200
CACCACCCAC CTCACTGTCT GTGTCAACCA CAGCAGGCTG GAGCAGTCAG CTCAGGAACA      1260
GGCAAAACCT TAGGTCCTCC GCCTACCTAA CCTTCAATAC ATCAAGGATA GGCTTCTTTG      1320
CTTGCCCCAA CCTCGCCCCA GTCTAGACCA CCTGGGGATT CCCAGCTCAG GGCGAAAAGG      1380
AAGCCCCGAGA AGCATTCTGT AGAGGGAAAT CCTGCATGAG TGCGCCCCCT TTCGTTACTC      1440
CAACACATCC AGCAACCACT GAACTTGGCC GGGGAACACA CCTGGTCCTC ATGCACCAGC      1500
ATTGTGACCA TCAACGGAAA AGTACTATTG CTGCGACCCC GCCCCTTCCG CTACAACGCT      1560
TGGTCCGCCT GAATCCCGCC CCTTCCTCCG TTCCAGCCT CATCTTTTTC GTCGTGGACT      1620
CTCAGTGGCC TGGGTCCTGG CTGTTTCTA AGCACACCCT TGCATCTTGG TTCCCGCACG      1680
TGGGAGGCCC ATCCCGGCCT TGAGCACAAT GACCCGCGCT CCTCGTTGCC CCGCGGTGCG      1740
CTCTCTGCTG CGCAGCCGAT ACCGGGAGGT GTGGCCGCTG GCAACCTTTG TGCGGCGCCT      1800
GGGGCCCCG                                     1808

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..2651
 - (D) OTHER INFORMATION: /note= "preliminary sequence of B2.18 containing the genomic promoter region of mouse telomerase reverse transcriptase (mTRT)"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 2057
 - (D) OTHER INFORMATION: /note= "mouse telomerase reverse transcriptase (mTRT) cDNA start site"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 2087
 - (D) OTHER INFORMATION: /note= "mouse telomerase reverse transcriptase (mTRT) ORF start site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAACAAAGTC AATGAGGAAT GGCTGTGTTT CATCTTGACC ACTGAGAAGT AAAACCGGGT	60
GCAGTGATGT CCAAAAAGGC AAGGTGACAG CAGAGCGGAG GCCCAATCT AGAGCAGGGC	120
CTTCGGTTTG AATGGGGGAG ATCAAACGGG AGTTGGTTTC TGCCAGCACG TTGGGGTAGA	180
AGGTGGAACA TGAAAGGTCC CCGAGGATTT CGAGAGTCCA TAGGGGTAGC GACACCCGAG	240
GTCTTCTTTT TCACCTCCTT CCCTGCAGGG GAGATGACTT TTACCACAGT CGTTTATGGG	300
AAAGTTCTTA GGGGCAGCCC CTCCCCAAA AGGCTCTCCC TGGCCTCATG TTCAAAGCA	360
CAGCTTTTTA AAGCAGGCCT GTTAAGCACA AAGGATCCCG AATCCTGGCT TCATCGTTGG	420
CTGGTAGACA ACTTCCACTC GTTTTCCACT TCAGTTTCTT CTAACCTGTG TGTTATTTGA	480
TTCTGATGCT TGAACCCAGG GTTGTGTAGT CAGCAAGTGC TACCCCTCC TCCTCTTCTT	540
TGTTTTTTTG AGGCAGGGTC TCATTTTGCC CAAGTGGACC TAAATTTTCA CATGTAGCTG	600
GCCTGGTTTT GAATGCCTTC TCATCCTGCC TCTACTCCC AAGAGTAGCT TACAAGTGTG	660
CACCACCATG CCCCGCGATA TTCTTATTTT TGAGACTGTT TTCTATGCTG GTTTCTTTGG	720
GGAACTACAC TAAGGTAGCT TACAAGTGTG CACCACCATG CCCCGCGATA TTCTTATTTT	780
TGAGACTGTT TTCTATGCTG GTTCTTTTGG GGAACTACAC TAAGGTAGCT TCATTGTTGG	840
CATAAATTTT TCAGTTCAGG CCCATATCTC CTAAGTAGCA GAACTAAGCA AATCTCAAAC	900
AAACCCCTCA AAAAGACTGA TGTCCACTAA ACGGACTTCT AAAATAGCTC CCTGTAATCC	960
TGAGCATTTA CAAGGCGGCA GACCTCCTAT AAGGGAGTAA ATATGAAAAC GCGCCTGTTC	1020
AAATGCTAGG TCGGTGGATA GAAGCAATTT CCTCAGAAAG CTGAAGGCAC CAAAGGTTAT	1080
ATTTGTTAGC ATTTCAAGTGT TTGCCAACT CAGCTACAGT AGAGATCACA GATTCCCTAT	1140
TTCCCAGAGA TTCAAATTC AGCAGCCCCT CTCTAACTAT GGCTCAGAGT CGTGTCATTA	1200
CATATGCCCC AACAACAACC CCCACCCCTA TCCTACCCCC GCCTCACACG TGCAAGTACT	1260
ATCACAGTTG CCAACCTAGC AGAGCTGCCA TCCTAAGGTC GAGGTCGCCG CTTTGGCTGT	1320
GTGCACAGGC AAGCGCCCTC ACCCAATGGC CCTGGCCTTG CTATGGGTGC GTGAGTTGAG	1380
ATGATGCTCT GGAATCTGAG GTGAAGGCCA CTGGAACAGT GAAAAAAGCT AACGCAGGGC	1440
TTTTACCTAG GTCCCCTTCC TTTGGTGGTG GGTGTTTACG GAACATATTT GGGATCTGGA	1500
GTGTATGGTC GCACCACAAT AAAGCCTTAA CCTATATAGT AGAATTTTCA CTGTAATCAT	1560
TAAGAACTGA GATTGCCACC ACCCACCTCA CTGTCTGTGT CAACCACAGC AGGCTGGAGC	1620
AGTCAGCTCA GGAACAGGCA AAACCTTAGG TCCCTCCGCC TACCTAACCT TCAATACATC	1680
AAGGATAGGC TTCTTTGCTT GCCCAAACCT CGCCCCAGTC TAGACCACCT GGGGATTCCC	1740
AGCTCAGGGC GAAAAGGAAG CCCGAGAAGC ATTCTGTAGA GGGAAATCCT GCATGAGTGC	1800
GCCCCCTTTC GTTACTCCAA CACATCCAGC AACCCTGAA CTTGGCCGGG GAACACACCT	1860
GGTCCCTCATG CACCAGCATT GTGACCATCA ACGGAAAAGT ACTATTGCTG CGACCCCGCC	1920
CCTTCCGCTA CAACGCTTGG TCCGCCTGAA TCCCGCCCCT TCCTCCGTTC CCAGCCTCAT	1980

CTTTTTCGTC GTGGACTCTC AGTGGCCTGG GTCCTGGCTG TTTTCTAAGC ACACCCTTGC 2040
 ATCTTGGTTC CCGCACGTGG GAAGGCCCAT CCCGGCCTTG AGCACAATGA CCCGCGCTCC 2100
 TCGTTGCCCC GCGGTGCGCT CTCTGCTGCG CAGCCGATAC CGGGAGGTGT GGCCGCTGGC 2160
 AACCTTTGTG CGGCGCCTGG GGCCCCAGGG CAGGCGGCTT GTGCAACCCG GGGACCGAAG 2220
 ATCTACCGCA CTTTGGGTG CCCAATGCCT AGTGTGCATG CACTGGGGCT CACAGCCTCC 2280
 ACCTGCCGAC CTTTCCTTCC ACCAGGTGGG CCTCCAGGCG GGATCCCCAT GGGTCAGGGG 2340
 CGGAAAGCCG GGAGGACGTG GGATAGTGCG TCTAGCTCAT GTGTCAAGAC CCTCTTCTCC 2400
 TTACCAGGTG TCATCCCTGA AAAGAGCTGG TGGCCAGGGT TGTGCAGAGA CTCTGCGAGC 2460
 GCAACGAGAG AAACGTGCTG GCTTTTGGCT TTGAGCTGCT TAACGAAGCC AGAAGCGGGC 2520
 CTCCCATGGC CTTACTAAT TAGCGTGCGT AAGCTACTTG CCCAACACTG TTATTGAAAA 2580
 CCTGCGTGTC AGTGGTGCAT GGATGCTACT GTTGAGCCGA ATGGGCGACA CCTGCTGGTC 2640
 TACCTGCTGG C 2651

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..18
 (D) OTHER INFORMATION: /note= "human telomerase reverse transcriptase (hTERT) substrate oligonucleotide "TS""

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATCCGTCGA GCAGAGTT

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..6
 (D) OTHER INFORMATION: /note= "human telomeric repeat"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTAGGG

6

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "3' primer hTRT.28"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCGGACCAG GGTCTGAGG AA

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "primer mTRT.35"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTCCTCAGG ACCCTGGTCC GAG

23

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "primer mTRT.27"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
ATTGAGGTCT GGGCATACCT GC

22

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..22
 (D) OTHER INFORMATION: /note= "3' primer encoding
 carboxy-terminus of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
TCAGCGTCGT CCCCGGAGC TT

22

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..22
 (D) OTHER INFORMATION: /note= "5' primer from upstream
 mTRT Ra-200"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
TCACCCTCTG AGGCTTCGGT GT

22

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /note= "primer mTRT.10"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
CGTCGATACT GGCAGATGCG G

21

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..24
 (D) OTHER INFORMATION: /note= "primer mTRT.53"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
GTGCTGAGGC TACAATGCCC ATGT

24

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /note= "5' primer mTRT.9"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
CTTTTACATC ACAGAGAGCA C

21

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..25
 (D) OTHER INFORMATION: /note= "primer mTRT.52"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATGTTTCATC TAGCGGAAGG AGACA

25

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: /note= "mF550A oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACAGCTGCTT AGATCTTTCG CTTACATCAC AGA

33

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "mD701A oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTGTTAAGGC AGCTGTGACC GGTGCCTATG ATGCC

35

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: /note= "mD860A oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
TACGTTTTGT TGCTGACTTT CTACTAGTGA CGCCTCAC

38

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..38
 (D) OTHER INFORMATION: /note= "mD600A oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCATCACCA GGCCACGTGG CTGGCCATGC CCATC

35

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr
1				5					10					15	
Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys
		20					25						30		
Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	Lys
		35				40						45			

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu	Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg
1				5					10					15	

Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
 20 25 30
 Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
 35 40 45
 Arg Leu Thr Ser Arg Val
 50

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 1 5 10 15
 Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 20 25 30
 Lys Pro

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser
 1 5 10 15
 Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe
 20 25 30
 Ala Gly Ile
 35

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 1 5 10 15
 His

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
 1 5 10 15
 Cys Val Val Asn Leu Arg Lys Thr Val Val
 20 25

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Trp Leu Met Asp Thr Tyr Val Val Gln Leu Leu Arg Ser Phe Phe Tyr
 1 5 10 15
 Ile Thr Glu Ser Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys
 20 25 30
 Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Val Arg Gln His Leu Glu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Glu Val Arg His His Gln Asp Thr Trp Leu Ala Met Pro Ile Cys Arg
 1 5 10 15
 Leu Arg Phe Ile Pro Lys Pro Asn Gly Leu Arg Pro Ile Val Asn Met
 20 25 30
 Ser Tyr Ser Met Gly Thr Arg Ala Leu Gly Arg Arg Lys Gln Ala Gln
 35 40 45
 His Phe Thr Gln Arg Leu
 50

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gln Thr Pro Arg Met Tyr Phe Val Lys Ala Asp Val Thr Gly Ala Tyr
 1 5 10 15
 Asp Ala Ile Pro Gln Gly Lys Leu Val Glu Val Val Ala Asn Met Ile
 20 25 30
 Arg His

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Arg Cys Tyr Thr Gln Cys Gln Gly Ile Pro Gln Gly Ser Ser Leu Ser
 1 5 10 15
 Thr Leu Leu Cys Ser Leu Cys Phe Gly Asp Met Glu Asn Lys Leu Phe
 20 25 30

Ala Glu Val
35

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Leu Leu Arg Phe Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Asp
 1 5 10 15
 Gln

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Lys Thr Phe Leu Ser Thr Leu Val His Gly Val Pro Glu Tyr Gly
 1 5 10 15
 Cys Met Ile Asn Leu Gln Lys Thr Val Val
 20 25

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

His Cys Leu Phe Pro Trp Cys Gly Leu Leu Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
 1 5 10 15
 Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 20 25 30
 Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
 1 5 10 15
 Leu Arg Leu Ile Pro Lys Lys Thr Thr
 20 25

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp Arg
 1 5 10 15
 Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn
 20 25

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 1 5 10 15
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 20 25 30
 Leu Leu

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser
 1 5 10 15
 Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu
 20 25 30
 Gly Phe Leu
 35

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn
 1 5 10 15
 Asn

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	Ile	Asn	Val	Ser	Arg	Glu	Asn	Gly
1				5					10					15	
Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	Thr						
			20					25							

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gln	Asp	Tyr	Cys	Asp	Trp	Ile	Gly	Ile	Ser	Ile
1				5					10	

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Trp	Leu	Phe	Arg	Gln	Leu	Ile	Pro	Lys	Ile	Ile	Gln	Thr	Phe	Phe	Tyr
1				5					10					15	
Cys	Thr	Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe	Arg	His	Asp
			20					25					30		
Thr	Trp	Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile	Val	Glu	Tyr	Phe	Lys	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Cys	Arg	Asn	His	Asn	Ser	Tyr	Thr	Leu	Ser	Asn	Phe	Asn	His	Ser	Lys
1				5					10					15	
Met	Arg	Ile	Ile	Pro	Lys	Lys	Ser	Asn	Asn						
			20					25							

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
 1 5 10 15
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro
 20 25

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
 1 5 10 15
 Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
 20 25 30
 Lys Asn

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser
 1 5 10 15
 Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser
 20 25 30
 Glu Phe Lys
 35

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
1 5 10 15
Gln

(2) INFORMATION FOR SEQ ID NO:49:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr Asn
1 5 10 15
Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala
20 25

(2) INFORMATION FOR SEQ ID NO:50:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Lys Glu Leu Glu Val Trp Lys His Ser Ser Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:51:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr
 1 5 10 15
 Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys
 20 25 30
 Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met
 35 40 45

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr Leu Pro Pro Ala Val
 1 5 10 15
 Ile Arg Leu Leu Pro Lys Lys Asn Thr
 20 25

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly
 1 5 10 15
 Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser
1 5 10 15

Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu
20 25 30

Ser Phe Thr
35

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His Asn
1 5 10 15

Phe Ser Thr Ser Leu Glu Lys Thr Val Ile
20 25

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Tyr Tyr Arg Lys
1

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Ile Pro Gln
1

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Asp Asp Phe Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Leu"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 10
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 11
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 12
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or Gln"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 13
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 2
      (D) OTHER INFORMATION: /product= "OTHER"
                             /note= "Xaa = Ile or Leu"
```

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe or Trp or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Arg or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 25
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Tyr or Phe"

- (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

(2) INFORMATION FOR SEQ ID NO:64:

(A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Xaa Arg Xaa Xaa Pro Lys Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Xaa Arg Xaa Ile Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = charged amino acid
 selected from Asp, Glu, His, Lys or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Tyr or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Cys or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Pro Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa
 1 5 10 15
 Xaa

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ile or Leu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Pro or Phe"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ser or Leu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Val"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 16
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 17
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Tyr	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Gln	Gly	Xaa	Xaa	Xaa	Ser	Xaa	Xaa
1				5					10					15	
Xaa															

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ile or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Met"

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 3
      (D) OTHER INFORMATION: /product= "OTHER"
                               /note= "Xaa = Arg or Lys"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 4
      (D) OTHER INFORMATION: /product= "OTHER"
                               /note= "Xaa = hydrophobic amino acid
                               selected from Ala, Leu, Ile, Val, Pro,
                               Phe, Trp or Met"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 8
      (D) OTHER INFORMATION: /product= "OTHER"
                             /note= "Xaa = Tyr or Phe"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 10
      (D) OTHER INFORMATION: /product= "OTHER"
                               /note= "Xaa = hydrophobic amino acid
                                     selected from Ala, Leu, Ile, Val, Pro,
                                     Phe, Trp or Met"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 11
      (D) OTHER INFORMATION: /product= "OTHER"
                               /note= "Xaa = Ile or Val"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 12
      (D) OTHER INFORMATION: /product= "OTHER"
                             /note= "Xaa = Thr or Ser"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Asp	Xaa	Leu	Xaa	Xaa	Xaa
1				5				10			

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

(2) INFORMATION FOR SEQ ID NO:70:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Trp or Phe"

(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gly or His"

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Tyr or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Tyr or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1           5           10           15
Val Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
20           25           30
Xaa Trp

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ile or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Arg or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 25
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Tyr or Phe"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 30
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Tyr or Phe"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 32
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Tyr
1				5				10							15	
Val	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	
			20					25						30		
Xaa	Xaa	Trp														
			35													

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ile or Leu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Xaa Arg Xaa Xaa Pro Lys Xaa Asp Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Tyr or Phe"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Cys or Ala"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 17
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ile or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Pro Glu Xaa Xaa Phe Xaa Xaa Val Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa
 1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or Gln"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Leu"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Pro or Phe"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 11
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Leu"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 13
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Val"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 16
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 17
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Leu"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Tyr	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Gln	Gly	Xaa	Ile	Xaa	Ser	Xaa	Xaa
1				5				10						15	
Xaa															

- ```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ile or Leu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Arg or Lys"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Tyr or Phe"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ile or Val"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Thr or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
Xaa Xaa Xaa Leu Xaa Asp Asp Xaa Leu Xaa Xaa Xaa
1 5 10

```

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Gly or Val"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 4
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = charged amino acid  
selected from Asp, Glu, His, Lys or Arg"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 6
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = polar amino acid  
selected from Gly, Ser, Thr, Tyr, Cys,  
Asn or Gln"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 10
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Asn or Ser"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:
 

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Arg | Lys | Xaa | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 2
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Ile or Leu"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 12  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Arg or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = polar amino acid  
 selected from Gly, Ser, Thr, Tyr, Cys,  
 Asn or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 21  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = polar amino acid  
 selected from Gly, Ser, Thr, Tyr, Cys,  
 Asn or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 25  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = polar amino acid  
 selected from Gly, Ser, Thr, Tyr, Cys,  
 Asn or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 28  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Tyr or Phe"

(A) NAME/KEY: Modified-site  
(B) LOCATION: 29  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Tyr or Phe"

(A) NAME/KEY: Modified-site  
(B) LOCATION: 31  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Lys or His"

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(A) NAME/KEY: Modified-site  
(B) LOCATION: 2  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Ile or Leu"

(A) NAME/KEY: Modified-site  
(B) LOCATION: 7  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(A) NAME/KEY: Modified-site  
(B) LOCATION: 8  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(A) NAME/KEY: Modified-site  
(B) LOCATION: 10  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

- (ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Xaa Xaa Trp  
35

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 3
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 4
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Ile or Leu"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 9
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = polar amino acid  
selected from Gly, Ser, Thr, Tyr, Cys,  
Asn or Gln"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Xaa Arg Xaa Xaa Pro Lys Xaa Asn Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 4
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Tyr or Phe"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Cys or Ala"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 17  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Ile or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Xaa | Xaa | Phe | Xaa | Xaa | Asp | Asp | Xaa | Xaa | Xaa | Xaa | Tyr | Asp | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Arg or Gln"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Ile or Leu"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Pro or Phe"



(A) NAME/KEY: Modified-site  
(B) LOCATION: 11  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Ser or Leu"

(A) NAME/KEY: Modified-site  
(B) LOCATION: 13  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Leu or Val"

```
(A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"
```

(A) NAME/KEY: Modified-site  
(B) LOCATION: 17  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Ile or Leu"

Tyr Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Gly Xaa Ser Xaa Ser Xaa Xaa  
1 5 10 15  
Xaa

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Ile or Leu"

(A) NAME/KEY: Modified-site  
(B) LOCATION: 2  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Leu or Met"

(A) NAME/KEY: Modified-site  
(B) LOCATION: 3  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Arg or Lys"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Tyr or Phe"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid  
 selected from Ala, Leu, Ile, Val, Pro,  
 Phe, Trp or Met"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Ile or Val"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 12  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Leu or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Phe | Xaa | Asp | Asp | Xaa | Leu | Xaa | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Gly or Val"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = charged amino acid  
 selected from Asp, Glu, His, Lys or Arg"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = polar amino acid  
 selected from Gly, Ser, Thr, Tyr, Cys,  
 Asn or Gln"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Lys Xaa Xaa Xaa  
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

- (ix) FEATURE:

- (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Xaa Xaa Asp Asp Xaa  
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Phe or Tyr"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Xaa Xaa Asp Asp Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Trp Xaa Gly Xaa  
1

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Xaa Leu Gly Xaa Xaa Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr  
 1 5 10 15  
 Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa  
 20 25 30  
 Xaa Trp

## (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr  
 1 5 10 15  
 Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa  
 20 25 30  
 Xaa Xaa Trp  
 35

## (2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Leu or Ile"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 12  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Gln or Arg"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 28  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Phe or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 29  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Phe or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 31  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Phe | Phe | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Xaa | Thr | Glu | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Arg | Xaa | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Xaa | Trp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = Leu or Ile"



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Xaa Arg Xaa Ile Pro Lys Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Xaa Arg Xaa Ile Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa  
1 5 10 15  
Xaa



## (2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 6
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 8
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 10
  - (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Pro Xaa Leu Tyr Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa  
 1                      5                      10                      15  
 Ile

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Tyr Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa  
 1                      5                      10                      15  
 Xaa Xaa Xaa Xaa Xaa Xaa  
 20

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid  
selected from Ala, Leu, Ile, Val, Pro,  
Phe, Trp or Met"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Gln Xaa Xaa Gly Ile Pro Gln Gly Ser Xaa Leu Ser Xaa Xaa Leu  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Leu Leu Arg Phe Xaa Asp Asp Phe Leu Leu Xaa Thr  
 1                      5                      10

a 4  
cont